

14. A host cell transformed or transfected with the expression vector of claim 11.
15. A host cell transformed or transfected with the expression vector of claim 12.
16. A host cell transformed or transfected with the expression vector of claim 13.

Remarks

Claim 7 has been cancelled. Claims 1-6 and 8-16 are currently pending. Claims 1, 6 and 8-10 have been amended herewith.

Claim 1 has been amended to recite a RIP activity selected from the group consisting of DNA binding, protein multimerization, and nucleic acid looping. Support for this amendment can be found throughout the specification and particularly at page 21, lines 24-27.

Claim 1 is further amended to recite stringent conditions as described in the specification. Support for this amendment can be found on page 22, lines 18-24.

Claims 6 and 9-10 has been amended to remove the term "unique."

Claim 6 has been further amended to remove the negative provision objected to by the Examiner.

Claims 8 and 9 have been amended to correct claim dependency.

The specification has been amended to recite "0.015M" rather than "0.15M" sodium citrate in the composition of hybridization buffer component SSC. This was an inadvertent typographical error. Support for this amendment can be found in any standard molecular biology textbook such as Current Protocols in Human Genetics (Appendix A.2D.8) which teaches the composition of 20x SSC to be 3 M NaCl and 0.3M sodium citrate. The recitation of stringent conditions in claim 1, as now amended, includes this amendment.

No new matter has been added.

Rejection under 35 U.S.C. §112, first paragraph

The Examiner has maintained his rejection of claims 1-16 under 35 U.S.C. §112, first paragraph as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s) at the time the application was filed had possession of the claimed invention.

According to the Examiner, the specification does not adequately describe what the terms “RIP activity” or “stringent conditions” encompass.

Applicants have amended claim 1 to further define the terms “RIP activity” and “stringent conditions” as provided by the specification. (See page 21, lines 24-27, and page 22, lines 18-24.)

In view of these amendments, Applicants respectfully request that the Examiner reconsider and withdraw his rejection of now pending claims 1-6 and 8-16 under 35 U.S.C. §112, first paragraph.

Rejection under 35 U.S.C. §112, second paragraph

The Examiner has rejected claims 1, 6 and 9-10 under 35 U.S.C. §112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner has maintained his rejection of claim 1 in view of the recitation of the term “RIP60 activity” because, as stated previously, “it is unclear which RIP60 activity Applicant is referring to.” Applicants have amended claim 1 to further define RIP60 activity. (See page 21, lines 24-27.)

The Examiner has also maintained his rejection of claim 1 in view of the recitation of the term “under stringent conditions” because, as stated previously, the term is ambiguous. Applicants have further amended claim 1 to include the stringent conditions recited in the specification. (See page 22, lines 9-18.)

Accordingly, in view of these amendments, claim 1 is considered definite.

The Examiner has maintained his rejection of claim 6 in view of the recitation of the term “sequences having the database accession numbers of Table 1.” Claim 6 is further rejected because the limitation “other than the exact sequence” is a negative limitation. Applicants have amended the claim to remove the provision of the negative limitation in its entirety. This amendment does not narrow the scope of the claim.

The Examiner has maintained his rejection of claims 6 and 9-10 because of the recitation of the term “unique fragment.” Applicants have amended claims 6 and 9-10 to remove the term “unique.” This amendment does not narrow the scope of the claim.

Accordingly, in view of these amendments, claims 6 and 9-10 are considered definite.

In view of the foregoing, Applicants respectfully request that the Examiner reconsider and withdraw the rejection of claims 1, 6, and 9-10 under 35 U.S.C. §112, second paragraph.

Rejection under 35 U.S.C. §102(a)

The Examiner has maintained his rejection of claims 1-3 and 6-9 under 35 U.S.C. §102(a) in view of Sulston et al. (Genome Research, 8(11):1097-1108, 1998). Previously, the Examiner stated that the Sulston et al. reference discloses the polynucleotide sequences reciting SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:50. The Examiner now states that “the date of publication disclosed in the Genbank listing is prior to Applicant’s priority date (1998)” but that the dates upon which the sequences disclosed in the GenBank listing (Accession Number AC005586, in its present form, as relied on by the Examiner) “were publicly available ... are currently being determined.”

Applicants respectfully traverse the rejection for the reasons stated below.

The Sulston et al. reference was published in November 1998. It provides no explicit sequence information. It does, however, refer to sequence data posted at the Sanger website. The Examiner has not provided the sequence that was made available by Sulston et al. as of November 1998 on the Sanger website. The Examiner has provided a GenBank listing for the sequence having Accession Number AC005586 submitted by Sulston et al. which is reported to be the complete sequence of the Homo Sapiens PAC clone RP4-584D14 from chromosome region 7q31-q35, having a length of 132150 nucleotides. The GenBank listing (the front page of which is attached hereto as Appendix B) indicates that the sequence, in the form presented and relied upon by the Examiner, was made publicly available by GenBank on September 30, 2000 (see A). Accordingly, the nucleotide sequence cited and relied upon by the Examiner is not prior art because it was made publicly available (in the form cited by the Examiner) only after the priority date of the present application (i.e., January 1999).

Applicants found and herewith provide the revision history for Accession Number AC005586, and sequence data submitted to GenBank by Sulston et al. prior to the priority date of the present application. (See Appendices C-1 and C-2.) The revision history indicates that the sequence was first deposited with GenBank on September 1, 1998, with subsequent sequence revisions submitted on November 22, 1998, June 12, 2000, and September 30, 2000.

The September 1998 deposit, the earliest deposit, is a working draft of the Homo Sapiens clone DJ0584D14, and it consists of 18 arbitrarily ordered contigs with 17 gaps of unknown size

therebetween. The November 1998 deposit is also a working draft of the same clone, and it consists of 3 arbitrarily ordered contigs with 2 gaps of unknown size therebetween.

Notwithstanding that the Examiner has not met his burden of proof of establishing that the Sulston et al. references anticipate the subject matter of the pending claims, Applicants provide herewith, as Appendix D, a Declaration under 37 C.F.R. §1.131 of Nicholas H. Heintz, one of the co-inventors of the present application. The Declaration sets forth proof that Applicants had conception and reduction to practice of the subject matter of the rejected claims prior to the publication date of the Sulston GenBank submission in September 1998. Attached to the Declaration is Exhibit 1, the RIP60 nucleic acid sequence possessed by the inventor prior to September 1998; Exhibit 2, the RIP60 nucleic acid sequence as filed in the present invention; and Exhibit 3, a comparison of the sequences of Exhibits 1 and 2. Accordingly, Applicants believe that the rejection of claims 1-3 and 6-9 is obviated.

In view of the foregoing, Applicants respectfully request that the Examiner reconsider and withdraw the rejection of claims 1-3 and 6-9 under 35 U.S.C. §102(a) as being anticipated by Sulston et al. (Genome Research, 8(11):1097-1108, 1998).

Rejection under 35 U.S.C. §103(a)

The Examiner has maintained his rejection of claims 1-16 under 35 U.S.C. §103(a) as being unpatentable over Sulston et al. (Genome Research, 8(11):1097-1108, 1998). Previously, the Examiner stated that Sulston et al. disclose "the polynucleotide sequences recited SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and 50 (and) consequently, said reference anticipates all the limitations of the instant claims". The Examiner further stated that although "Sulston et al. does not explicitly disclose incorporating said polynucleotides with a promoter in an expression vector, transfecting a host cells with said vector nor using said transformed cell to express the recombinant proteins recited in the instant claims ... it would be obvious to one of skill in the art to take a polynucleotide sequence, determine the open reading frames and incorporate it in a vector so the polypeptide encoded by said polynucleotide can be expressed cheaply and efficiently in a recombinant system."

Applicants respectfully traverse the rejection for the same reasons stated above under the 102(a) rejection.

In view of the foregoing, Applicants respectfully request that the Examiner reconsider and withdraw the rejection of now pending claims 1-6 and 8-16 under 35 U.S.C. §103(a) as being unpatentable over Sulston et al. (Genome Research, 8(11):1097-1108, 1998).

Summary

Applicants believe that each of the pending claims now is in condition for allowance. If the Examiner has any questions and believes that a telephone conference with Applicants' representative would prove helpful in expediting the prosecution of this application, the Examiner is urged to call the undersigned at (617) 720-3500 (ext. 266).

Respectfully submitted,



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Attorney's Docket No.: V0139/7038 (HCL/MAT)
Date: February 8, 2002
x02/09/02

APPENDIX A:**MARKED-UP SPECIFICATION**

Please re-write the paragraph beginning on page 22, line 9, as follows (*noting that the new text has been indicated with a double underline to distinguish it from text that was original present in an underlined form and thus unchanged*):

Homologs and alleles of the RIP60 nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for RIP60 polypeptides and which hybridize to a nucleic acid molecule consisting of the coding region of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 or SEQ ID NO:50 under stringent conditions. The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. Molecular Cloning: A Laboratory Manual, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or Current Protocols in Molecular Biology, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH₂PO₄(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/[0.15M] 0.015M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed at 2x SSC at room temperature and then at 0.1x SSC/0.1% SDS at temperatures up to 68°C.

MARKED-UP CLAIMS

Please cancel claim 7. Please re-write the claims as shown below. A marked-up copy of the claims is attached to the end of this amendment as Appendix A.

1. (Twice Amended) An isolated nucleic acid molecule, comprising
 - (a) a nucleic acid molecule which hybridizes under stringent conditions to a molecule consisting of a nucleic acid of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:50 and which codes for a polypeptide having a RIP60 activity selected from the group consisting of DNA binding, protein multimerization, and nucleic acid looping,
 - (b) a nucleic acid molecule that differs from the nucleic acid molecule of (a) in codon sequence due to the degeneracy of the genetic code, and
 - (c) complements of (a) or (b),wherein the stringent conditions are hybridization at 65°C in hybridization buffer (3.5x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH₂PO₄ (pH7), 0.5% SDS, 2mM EDTA); wherein SSC is 0.15M sodium chloride/0.015M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid.
2. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule comprises SEQ ID NO:1.
3. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule comprises SEQ ID NO:3, SEQ ID NO:5 or SEQ ID NO:50.
4. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule codes for a polypeptide comprising SEQ ID NO:2.
5. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule codes for a polypeptide comprising SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:51.
6. (Twice Amended) An isolated nucleic acid molecule selected from the group consisting of
 - (a) a [unique] fragment of nucleic acid molecule of SEQ ID NO:1, and

(b) complements of (a)[,

provided that the unique fragment includes a sequence of contiguous nucleotides other than the exact sequence of any sequence selected from the sequence group consisting of

(1) sequences having the database accession numbers of Table 1, as published prior to January 4, 1999,

(2) complements of (1), and

(3) fragments of (1) and (2)].

8. (Amended) The isolated nucleic acid molecule of claim 6 [or 7], wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20[,] nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

9. (Amended) The isolated nucleic acid molecule of claim 6 [or 7], wherein the [unique] fragment encodes a peptide which is a fragment of a polypeptide consisting of SEQ ID NO:2.

10. (Amended) The isolated nucleic acid molecule of claim 8, wherein the [unique] fragment encodes a peptide which is a fragment of a polypeptide consisting of SEQ ID NO:2.

11. An expression vector comprising the isolated nucleic acid molecule of claims 1, 2, 3, 4 or 5 operably linked to a promoter.

12. An expression vector comprising the isolated nucleic acid molecule of claim 9, operably linked to a promoter.

13. An expression vector comprising the isolated nucleic acid molecule of claim 10, operably linked to a promoter.

14. A host cell transformed or transfected with the expression vector of claim 11.

15. A host cell transformed or transfected with the expression vector of claim 12.

16. A host cell transformed or transfected with the expression vector of claim 13.



PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Search for

Go

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Limits

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Add to Clipboard

☐ 1: [AC005586](#) **Homo sapiens PAC clone RP4-584D14 from 7q31-q35, complete sequence**

PubMed. Related Sequences. TaxonomyLinkOut

LOCUS AC005586 132150 bp DNA PRI 30-SEP-2000
 DEFINITION Homo sapiens PAC clone RP4-584D14 from 7q31-q35, complete sequence
 ACCESSION AC005586
 VERSION AC005586.2 GI:8468933
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 132150)
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE [99063792](#)
 REFERENCE 2 (bases 1 to 132150)
 AUTHORS Stoneking, T., Ozersky, P., Wohldmann, P. and Le, T.
 TITLE The sequence of Homo sapiens PAC clone RP4-584D14
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 132150)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1998) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE 4 (bases 1 to 132150)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE 5 (bases 1 to 132150)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (30-SEP-2000) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Jun 12, 2000 this sequence version replaced [gi:3907529](#).

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_DJ0584D14

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate

RECEIVED

JUL 31 2001

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JUL 26 2001

MARK OFFICE

Appendix B

Attch. to #10

CGCTCAGGATACGACTTCCTCCGCTAGAGATCGGATCCCCGGGCTATTATATAGCTCGATCGATC
 TTCTCTATATCCGCGATATGGGATATATACACACACACGCGCGGATAGCATGACTGATCT#
 CCCCATCT#
 CACAGACTTACGCT#

Nucleotide

chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GTB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP5-820A21, 200 base pair overlap. Actual start of this clone is at base position 1 of RP4-584D14; actual end is at base position 131954 of RP4-584D14.

The sequence RP4-584D14 from base position 21655 to 22775 is GT rich. This region was sized with PCR from genomic DNA and the hindiii digest with band size 3643 real, and 3642 insilico. The sequence RP4-584D14 from base position 22628 to 22637 is represented by sequence derived by PCR from genomic DNA.

FEATURES	Location/Qualifiers
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misc feature 9804..10293
 /note="similar to EST AI570541 (NID:g4533915) tm77h03.x1"
misc feature 9804..10155
 /note="similar to EST AW005172 (NID:g5853950) wz84b01.x1"
misc feature 9804..10168
 /note="similar to EST AA262035 (NID:g1898226) zs21e01.s1"
misc feature 9804..10266
 /note="similar to EST AA478979 (NID:g2205342) zu39b04.s1"
misc feature 9804..10266
 /note="similar to EST AI274899 (NID:g3897173) qk61h06.x1"
misc feature 9805..9954
 /note="similar to EST AI242577 (NID:g3837974) qi17e02.x1"
misc feature 9805..10317
 /note="similar to EST AW027740 (NID:g5886496) wv75g08.x1"
misc feature 9805..10068
 /note="similar to EST AI383384 (NID:g4196165) tc97a05.x1"
misc feature 9805..10110
 /note="similar to EST AA662653 (NID:g2616644) nu99h04.s1"
misc feature 9805..10140
 /note="similar to EST AI660300 (NID:g4763870) we66a08.x1"
misc feature 9805..10521
 /note="similar to EST AI014570 (NID:g3228951) ou40h08.x1"
misc feature 9806..10020
 /note="similar to EST W93039 (NID:g1422210) zd93e04.s1"
misc feature 9806..10277
 /note="similar to EST H96782 (NID:g1110268) yw98b03.s1"
misc feature 9807..10159
 /note="similar to EST AA975613 (NID:g3151405) oq41f09.s1"
misc feature 9807..10266
 /note="similar to EST AA909314 (NID:g3048719) om34b11.s1"
misc feature 9815..10451
 /note="similar to EST AI631828 (NID:g4683158) wa36f05.x1"
misc feature 9820..10162
 /note="match to EST AA813953 (NID:g2883549) oc06f02.s1"
misc feature 9820..10338
 /note="similar to EST AA742283 (NID:g2784283) ny28f10.s1"
misc feature 9820..10291
 /note="match to EST AA806412 (NID:g2875162) oc27c10.s1"
misc feature 9836..10388
 /note="similar to EST AW303355 (NID:g6713035) xv18b02.x1"
misc feature 9843..10365
 /note="similar to EST AA837494 (NID:g2912693) od20h07.s1"
repeat region 10001..10048
 /rpt_family="GC_rich"
misc feature 10037..10468
 /note="match to EST AA478214 (NID:g2206848) zu40f07.r1"
misc feature 10066..10068
 /note="match to EST R06319 (NID:g756939) yf08c08.r1"
misc feature 10081..10741
 /note="similar to EST AW411280 (NID:g6936821) fh11d05.x1"
misc feature 10314..10468
 /note="match to EST AA477916 (NID:g2206550) zu39b04.r1"
misc feature 10355..10697
 /note="similar to Mus musculus EST AA981950 (NID:g3160719) ua37c04.r1"
misc feature 10357..10890
 /note="match to EST AA280069 (NID:g1921543) zs93d12.r1"
misc feature 10544..10697
 /note="similar to EST AI242577 (NID:g3837974) qi17e02.x1"
misc feature 10601..10697
 /note="similar to Mus musculus EST W08046 (NID:g1282049) mb38c12.r1"
misc feature 10642..10701
 /note="match to EST R71963 (NID:g845995) yj84d08.r1"
misc feature 10778..10927
 /note="similar to EST AW016068 (NID:g5864825)"
misc feature 10845..11142

/note="match to EST AA077571 (NID:g1837045)"
misc feature 11044..11165
 /note="match to EST R71963 (NID:g845995) yj84d08.r1"
misc feature 11083..11373
 /note="similar to EST AW504279 (NID:g7141946)"
repeat region 11163..11290
 /rpt_family="MIR"
misc feature 11177..11433
 /note="similar to EST AI660300 (NID:g4763870) we66a08.x1"
misc feature 11390..11581
 /note="similar to EST AI373014 (NID:g4152880) qz02g01.x1"
misc feature 11390..11581
 /note="similar to EST AI934673 (NID:g5673543) wp87g08.x1"
misc feature 11632..11854
 /note="similar to EST AW075108 (NID:g6030106) xa68c07.x1"
misc feature 12057..12254
 /note="similar to Mus musculus EST W08046 (NID:g1282049)
 mb38c12.r1"
misc feature 12057..12254
 /note="match to EST R71963 (NID:g845995) yj84d08.r1"
misc feature 12663..13844
 /note="CpG_island (%GC=71.3, o/e=0.90, #CpGs=138)"
misc feature 12793..13135
 /note="similar to EST AL046625 (NID:g5434691)"
repeat region 12934..12980
 /rpt_family="GC_rich"
misc feature 12984..13111
 /note="similar to Mus musculus EST AA981950 (NID:g3160719)
 ua37c04.r1"
misc feature 12984..13040
 /note="match to EST R71963 (NID:g845995) yj84d08.r1"
misc feature 12984..13033
 /note="similar to EST AI242577 (NID:g3837974) qi17e02.x1"
misc feature 12984..13081
 /note="similar to Mus musculus EST W08046 (NID:g1282049)
 mb38c12.r1"
repeat region 13177..13246
 /rpt_family="GC_rich"
misc feature 13594..14074
 /note="similar to EST AI912005 (NID:g5631860) wd78f12.x1"
repeat region 14346..14501
 /rpt_family="L1"
repeat region 14619..14915
 /rpt_family="Alu"
repeat region 14987..14998
 /rpt_family="Alu"
repeat region 14999..15049
 /rpt_family="(TTTA)n"
repeat region 15050..15333
 /rpt_family="Alu"
repeat region 15622..16162
 /rpt_family="MER4-group"
misc feature 15702..15706
 /note="match to EST AA129215 (NID:g1689084) zn84b02.s1"
repeat region 16163..16456
 /rpt_family="Alu"
repeat region 16457..16620
 /rpt_family="MER4-group"
repeat region 16757..17068
 /rpt_family="Alu"
repeat region 17268..17501
 /rpt_family="MIR"
repeat region 18315..18407
 /rpt_family="L2"
misc feature 18483..18956
 /note="match to EST AA451648 (NID:g2165317) zx43e05.r1"
misc feature 18680..19256

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/note="similar to EST AW195520 (NID:g6474650) xn39e04.x1"
repeat_region 18830..19325
/rpt_family="MER21-group"
repeat_region 19711..19877
/rpt_family="L2"
repeat_region 19988..20144
/rpt_family="L2"
repeat_region 20148..20391
/rpt_family="MaLR"
repeat_region 20508..20671
/rpt_family="MER4-group"
repeat_region 20672..20711
/rpt_family="(TTTA)n"
repeat_region 20712..20989
/rpt_family="Alu"
repeat_region 20996..21103
/rpt_family="MER4-group"
repeat_region 21104..21371
/rpt_family="Alu"
repeat_region 21372..21413
/rpt_family="(TATATG)n"
repeat_region 21414..21663
/rpt_family="MER4-group"
repeat_region 21682..21859
/rpt_family="(TG)n"
repeat_region 22043..22274
/rpt_family="(TG)n"
repeat_region 22322..22497
/rpt_family="(GTGTG)n"
repeat_region 22610..22772
/rpt_family="(GTGTG)n"
repeat_region 22776..22953
/rpt_family="MER4-group"
repeat_region 22957..23066
/rpt_family="MaLR"
repeat_region 23107..23303
/rpt_family="L2"
repeat_region 23303..23390
/rpt_family="L2"
repeat_region 23480..23612
/rpt_family="Alu"
misc_feature 23519..23841
/note="match to EST T96609 (NID:g735233) ye51d03.s1"
misc_feature 23819..24212
/note="match to EST T96719 (NID:g735343) ye51d03.r1"
repeat_region 24755..24847
/rpt_family="(TTATA)n"
repeat_region 25094..25171
/rpt_family="HY4"
repeat_region 25343..25648
/rpt_family="Alu"
misc_feature 25347..25366
/note="similar to EST AA199876 (NID:g1795583) zq52f04.s1"
misc_feature 25360..25372
/note="match to EST AA805585 (NID:g2874285) oc18b08.s1"
repeat_region 25657..25793
/rpt_family="MaLR"
repeat_region 25992..26076
/rpt_family="LTR54"
repeat_region 26077..26277
/rpt_family="MER4-group"
repeat_region 26303..26696
/rpt_family="MER4-group"
repeat_region 26711..26894
/rpt_family="Alu"
repeat_region 26895..27166
/rpt_family="Alu"

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repeat_region 27167..27273
 /rpt_family="Alu"
repeat_region 27541..27614
 /rpt_family="L2"
misc_feature 27613..27619
 /note="similar to EST AA814848 (NID:g2884444) oc05g05.s1"
repeat_region 28006..28307
 /rpt_family="Alu"
repeat_region 28308..28386
 /rpt_family="Other"
repeat_region 28528..28642
 /rpt_family="Other"
repeat_region 28676..28965
 /rpt_family="Alu"
repeat_region 28974..29020
 /rpt_family="Other"
repeat_region 29045..29073
 /rpt_family="AT_rich"
repeat_region 29111..29426
 /rpt_family="Alu"
repeat_region 29454..29843
 /rpt_family="L1"
misc_feature 29607..29611
 /note="match to EST H11135 (NID:g875955) ym09b02.r1"
repeat_region 30041..30213
 /rpt_family="Alu"
repeat_region 30244..30313
 /rpt_family="L1"
repeat_region 30374..30757
 /rpt_family="L1"
repeat_region 30800..31053
 /rpt_family="Alu"
repeat_region 31106..31290
 /rpt_family="Alu"
repeat_region 31328..31477
 /rpt_family="L1"
repeat_region 31478..31774
 /rpt_family="Alu"
repeat_region 31775..31812
 /rpt_family="(TA)n"
repeat_region 31813..31979
 /rpt_family="L1"
repeat_region 31980..32280
 /rpt_family="Alu"
repeat_region 32281..32616
 /rpt_family="L1"
STS complement(32657..32879)
 /db_xref="GI:292544"
repeat_region 32823..32850
 /rpt_family="(TTTG)n"
repeat_region 32851..33014
 /rpt_family="Alu"
repeat_region 33135..33172
 /rpt_family="AT_rich"
repeat_region 33723..33933
 /rpt_family="MaLR"
repeat_region 33935..33973
 /rpt_family="(TTTA)n"
repeat_region 33974..34255
 /rpt_family="Alu"
misc_feature 34118..34133
 /note="match to EST AA582540 (NID:g2359900) nn55a06.s1"
repeat_region 34256..34366
 /rpt_family="MaLR"
repeat_region 34367..34655
 /rpt_family="Alu"
repeat_region 34656..34798

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/rpt_family="(GGAA)n"
repeat_region 34871..35653
/rpt_family="L2"
repeat_region 35663..35980
/rpt_family="Alu"
repeat_region 36021..36308
/rpt_family="Alu"
repeat_region 36559..36630
/rpt_family="MER1_type"
repeat_region 36632..36976
/rpt_family="MER1_type"
repeat_region 37028..37088
/rpt_family="Alu"
repeat_region 37089..37328
/rpt_family="Alu"
misc_feature 37206..37221
/note="match to EST AI144038 (NID:g3665847) qi63b05.x1"
misc_feature 37210..37221
/note="similar to EST AA031509 (NID:g1501463) zk13a09.s1"
misc_feature 37210..37221
/note="match to EST AI053787 (NID:g3321574) qi70a03.x1"
misc_feature 37210..37221
/note="match to EST AA835735 (NID:g2910054) od66f10.s1"
repeat_region 37339..37902
/rpt_family="MER1_type"
repeat_region 38075..38240
/rpt_family="L2"
repeat_region 38341..38425
/rpt_family="MER4-group"
repeat_region 38434..38549
/rpt_family="Alu"
repeat_region 38561..38667
/rpt_family="MER21-group"
repeat_region 38668..39015
/rpt_family="MER4-group"
repeat_region 39296..39414
/rpt_family="MIR"
misc_feature 39318..39364
/note="match to EST AA159496 (NID:g1735039) zo72b05.s1"
misc_feature 39365..39701
/note="match to EST AA159496 (NID:g1735039) zo72b05.s1"
misc_feature 39562..40154
/note="match to EST AA161506 (NID:g1735816) zo72b05.r1"
misc_feature 39983..41554
/note="CpG_island (%GC=69.3, o/e=0.70, #CpGs=111)"
repeat_region 40197..40329
/rpt_family="L2"
misc_feature 40234
/note="match to EST H84693 (NID:g1063912) ys70b04.r1"
misc_feature 40279..40347
/note="match to EST W07009 (NID:g1281013) za91f02.r1"
misc_feature 40281..40347
/note="match to EST H84693 (NID:g1063912) ys70b04.r1"
misc_feature 40285..40347
/note="match to EST AA297719 (NID:g1950053)"
misc_feature 40378..40380
/note="match to EST AA507194 (NID:g2243633) nh43f08.s1"
misc_feature 41237..41489
/note="similar to EST AW655938 (NID:g7421764)"
misc_feature 41282..41489
/note="similar to EST AW483984 (NID:g7054090)"
misc_feature 41296..41489
/note="match to EST H84693 (NID:g1063912) ys70b04.r1"
misc_feature 41296..41490
/note="match to EST AA297719 (NID:g1950053)"
misc_feature 41296..41489
/note="match to EST W07009 (NID:g1281013) za91f02.r1"

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misc feature 41303..41489
/note="match to EST W37661 (NID:g1319254) zc12e08.r1"
misc feature 41316..41489
/note="similar to EST AI301886 (NID:g3961232) qn56e01.x1"
misc feature 41351..41489
/note="similar to EST AI192960 (NID:g3744169) qe68g08.x1"
misc feature 41377..41489
/note="similar to EST AI953803 (NID:g5746113) wx69f03.x1"
misc feature 41424..41825
/note="match to EST AA481944 (NID:g2209622) zv43a07.r1"
misc feature 41427..41489
/note="similar to EST AI702025 (NID:g4989925) tq20d09.x1"
misc feature 41433..41774
/note="similar to EST AA292312 (NID:g1940308) zt51b01.r1"
misc feature 41462..41489
/note="similar to EST AI335981 (NID:g4072908) qt49g04.x1"
misc feature 41466..41488
/note="match to EST AA846256 (NID:g2932396) ai83g05.s1"
misc feature 41685..41825
/note="match to EST AA482067 (NID:g2209745) zv43a07.s1"
misc feature 41712..41825
/note="match to EST N62038 (NID:g1208189)"
misc feature 41720..41825
/note="match to EST AA995263 (NID:g3181752) os19g11.s1"
misc feature 41720..41825
/note="match to EST W37475 (NID:g1319136) zc12e08.s1"
misc feature 41721..41825
/note="similar to EST AW655938 (NID:g7421764)"
misc feature 41721..41825
/note="match to EST W37661 (NID:g1319254) zc12e08.r1"
misc feature 41721..41825
/note="similar to EST AI702025 (NID:g4989925) tq20d09.x1"
misc feature 41721..41825
/note="match to EST AA507194 (NID:g2243633) nh43f08.s1"
misc feature 41721..41825
/note="similar to EST AI953803 (NID:g5746113) wx69f03.x1"
misc feature 41721..41794
/note="match to EST H84693 (NID:g1063912) ys70b04.r1"
misc feature 41721..41825
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misc feature 41721..41825
/note="match to EST AA846256 (NID:g2932396) ai83g05.s1"
misc feature 41721..41825
/note="match to EST W07009 (NID:g1281013) za91f02.r1"
misc feature 41721..41825
/note="match to EST AI096654 (NID:g3446148) qb36a10.x1"
misc feature 41721..41825
/note="similar to EST AI192960 (NID:g3744169) qe68g08.x1"
misc feature 41721..41825
/note="similar to EST AI301886 (NID:g3961232) qn56e01.x1"
misc feature 41721..41825
/note="similar to EST AW483984 (NID:g7054090)"
misc feature 41737..41825
/note="match to EST AA449630 (NID:g2163380) zx08f01.r1"
misc feature 41796..41825
/note="similar to EST AI286253 (NID:g3924486) qu91a01.x1"
misc feature 42843..42939
/note="match to EST AA976115 (NID:g3151907) on33b08.s1"
misc feature 42844..42939
/note="match to EST AI096654 (NID:g3446148) qb36a10.x1"
misc feature 42844..42940
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misc feature 42844..42944
/note="match to EST W07009 (NID:g1281013) za91f02.r1"
misc feature 42844..42939
/note="similar to EST AI335981 (NID:g4072908) qt49g04.x1"
misc feature 42844..42939

misc feature /note="similar to EST AI286253 (NID:g3924486) qu91a01.x1"
42844..42939
misc feature /note="match to EST AA846256 (NID:g2932396) ai83g05.s1"
42844..42939
misc feature /note="similar to EST AI702025 (NID:g4989925) tq20d09.x1"
42844..42939
misc feature /note="match to EST W37475 (NID:g1319136) zc12e08.s1"
42844..42939
misc feature /note="match to EST AA482067 (NID:g2209745) zv43a07.s1"
42844..42939
misc feature /note="similar to EST AI301886 (NID:g3961232) qn56e01.x1"
42844..42939
misc feature /note="match to EST AA995263 (NID:g3181752) os19g11.s1"
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misc feature /note="similar to EST AI192960 (NID:g3744169) qe68g08.x1"
42844..42939
misc feature /note="match to EST AA449630 (NID:g2163380) zx08f01.r1"
42844..42939
misc feature /note="match to EST AA507194 (NID:g2243633) nh43f08.s1"
42844..42939
misc feature /note="match to EST N62038 (NID:g1208189)"
42844..42939
misc feature /note="match to EST AA481944 (NID:g2209622) zv43a07.r1"
42844..42939
misc feature /note="similar to EST AW655938 (NID:g7421764)"
42844..42939
misc feature /note="match to EST W37661 (NID:g1319254) zc12e08.r1"
42844..42939
misc feature /note="similar to EST AI953803 (NID:g5746113) wx69f03.x1"
42850..42939
misc feature /note="match to EST W60571 (NID:g1367548) zd26g05.r1"
42851..42939
misc feature /note="match to EST AA297373 (NID:g1949706)"
42862..42939
misc feature /note="similar to EST AI886213 (NID:g5591377) wm08a12.x1"
42889..42939
misc feature /note="similar to EST AW135940 (NID:g6140073)"
42896..42939
misc feature /note="match to EST AI092081 (NID:g3431075) qa93f01.s1"
43065..43067
misc feature /note="match to EST AA548797 (NID:g2319079) nk02f03.s1"
43184..43295
misc feature /note="similar to EST AI301886 (NID:g3961232) qn56e01.x1"
43184..43295
misc feature /note="match to EST AA995263 (NID:g3181752) os19g11.s1"
43184..43290
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43184..43257
misc feature /note="match to EST N62038 (NID:g1208189)"
43184..43269
misc feature /note="match to EST AA481944 (NID:g2209622) zv43a07.r1"
43184..43309
misc feature /note="match to EST W37661 (NID:g1319254) zc12e08.r1"
43184..43285
misc feature /note="similar to EST AW655938 (NID:g7421764)"
43184..43310
misc feature /note="similar to EST AI335981 (NID:g4072908) qt49g04.x1"
43184..43310
misc feature /note="similar to EST AI286253 (NID:g3924486) qu91a01.x1"
43184..43310
misc feature /note="similar to EST AI886213 (NID:g5591377) wm08a12.x1"
43184..43310
misc feature /note="match to EST AA846256 (NID:g2932396) ai83g05.s1"
43184..43310
misc feature /note="similar to EST AW135940 (NID:g6140073)"
43184..43310
misc feature /note="similar to EST AI702025 (NID:g4989925) tq20d09.x1"

misc feature 43184..43310
/note="match to EST AI096654 (NID:g3446148) qb36a10.x1"
misc feature 43184..43310
/note="match to EST W37475 (NID:g1319136) zc12e08.s1"
misc feature 43184..43310
/note="match to EST AA482067 (NID:g2209745) zv43a07.s1"
misc feature 43184..43310
/note="similar to EST AI192960 (NID:g3744169) qe68g08.x1"
misc feature 43184..43310
/note="match to EST AA976115 (NID:g3151907) on33b08.s1"
misc feature 43184..43310
/note="match to EST AA297373 (NID:g1949706)"
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/note="match to EST AA449630 (NID:g2163380) zx08f01.r1"
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/note="match to EST AA507194 (NID:g2243633) nh43f08.s1"
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/note="similar to EST AI953803 (NID:g5746113) wx69f03.x1"
misc feature 43211..43310
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misc feature 43240..43310
/note="match to EST AA614395 (NID:g2466591) np46e02.s1"
misc feature 43484..43595
/note="match to EST W60571 (NID:g1367548) zd26g05.r1"
misc feature 43486..43607
/note="similar to EST AI886213 (NID:g5591377) wm08a12.x1"
misc feature 43486..43600
/note="match to EST AA846256 (NID:g2932396) ai83g05.s1"
misc feature 43486..43602
/note="similar to EST AI702025 (NID:g4989925) tq20d09.x1"
misc feature 43486..43603
/note="match to EST AI096654 (NID:g3446148) qb36a10.x1"
misc feature 43486..43609
/note="match to EST AA482067 (NID:g2209745) zv43a07.s1"
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/note="similar to EST AI335981 (NID:g4072908) qt49g04.x1"
misc feature 43486..43596
/note="similar to EST AI286253 (NID:g3924486) qu91a01.x1"
misc feature 43486..43596
/note="similar to EST AW135940 (NID:g6140073)"
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/note="similar to EST AI192960 (NID:g3744169) qe68g08.x1"
misc feature 43486..43594
/note="match to EST AA976115 (NID:g3151907) on33b08.s1"
misc feature 43486..43594
/note="match to EST AA614395 (NID:g2466591) np46e02.s1"
misc feature 43486..43540
/note="match to EST AA297373 (NID:g1949706)"
misc feature 43486..43597
/note="match to EST AA548797 (NID:g2319079) nk02f03.s1"
misc feature 43486..43597
/note="match to EST W37475 (NID:g1319136) zc12e08.s1"
misc feature 43486..43597
/note="match to EST AA449630 (NID:g2163380) zx08f01.r1"
misc feature 43486..43599
/note="match to EST AA507194 (NID:g2243633) nh43f08.s1"
misc feature 43486..43595
/note="similar to EST AI953803 (NID:g5746113) wx69f03.x1"
misc feature 43767..44115
/note="match to EST AI144038 (NID:g3665847) qi63b05.x1"
misc feature 43769..43926
/note="similar to EST AI800018 (NID:g5365490) wc41f01.x1"
misc feature 43769..44049
/note="match to EST AA838544 (NID:g2913343) oe39c02.s1"
misc feature 43769..44231

misc feature /note="match to EST R51319 (NID:g813221) yg72f04.s1"
43769..43961
misc feature /note="match to EST AI053787 (NID:g3321574) qi70a03.x1"
43770..43878
misc feature /note="similar to EST AI937338 (NID:g5676208) wp76a04.x1"
43771..43952
misc feature /note="match to EST AA805535 (NID:g2874285) oc18b08.s1"
43772..44107
misc feature /note="similar to EST AI349626 (NID:g4086832) ta74h08.x2"
43775..44077
misc feature /note="match to EST N80586 (NID:g1243287) zb02e06.s1"
43775..44192
misc feature /note="match to EST R49133 (NID:g820202) yg69f08.s1"
43775..44090
misc feature /note="match to EST AA582540 (NID:g2359900) nn55a06.s1"
43777..44214
misc feature /note="match to EST H41438 (NID:g917490) yp72h06.s1"
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44227..44300
misc feature /note="match to EST N80586 (NID:g1243287) zb02e06.s1"
44228..44229
misc feature /note="match to EST R49133 (NID:g820202) yg69f08.s1"
44248..44536
misc feature /note="match to EST AA077645 (NID:g1837329)"
44257..44593
misc feature /note="similar to EST AI937338 (NID:g5676208) wp76a04.x1"
44563..45013
misc feature /note="match to EST R51431 (NID:g813333) yg72f04.r1"
44770..45207
misc feature /note="similar to EST AI807218 (NID:g5393784) wf38b11.x1"
44789..45175
misc feature /note="similar to EST AI807212 (NID:g5393778) wf38b05.x1"
44850..45207
misc feature /note="similar to EST AI821213 (NID:g5440292) ne09f10.y5"
44940..45197
misc feature /note="match to EST AA295306 (NID:g1947641)"
46869..47188
repeat region /rpt_family="Alu"
misc feature 46870..46897
46870..46897
repeat region /note="match to EST AA805365 (NID:g2874115) oc15f09.s1"
48454..48665
48454..48665
misc feature /rpt_family="MER1_type"
49193..49399
49193..49399
misc feature /note="match to EST AA805365 (NID:g2874115) oc15f09.s1"
49201..49448
49201..49448
misc feature /note="similar to EST AI702308 (NID:g4990208) tz36g12.x1"
49201..49609
49201..49609
misc feature /note="match to EST AI027467 (NID:g3244983) ow06c10.x1"
49201..49526
49201..49526
misc feature /note="match to EST AA835735 (NID:g2910054) od66f10.s1"
49204..49757
49204..49757
misc feature /note="similar to EST AI762857 (NID:g5178524) wi63b04.x1"
49204..49476
49204..49476
misc feature /note="similar to EST AI244028 (NID:g3839425) qj62c01.x1"
49204..49683
49204..49683
misc feature /note="similar to EST AI949997 (NID:g5742307) wq15d01.x1"
49672..49984
49672..49984
misc feature /note="match to EST AA169345 (NID:g1748303) zp17e12.s1"
50192..50536
50192..50536
misc feature /note="match to EST T81965 (NID:g704972) yd94h11.r1"
50695..50700
50695..50700
misc feature /note="match to EST H41438 (NID:g917490) yp72h06.s1"

misc feature 52748..52893
 /note="similar to EST AA199876 (NID:g1795583) zq52f04.s1"
misc feature 52753..52893
 /note="similar to EST AA207191 (NID:g1802683) zq73f05.r1"
misc feature 53464..53889
 /note="similar to EST AA121611 (NID:g1679226) zn78c08.r1"
misc feature 53924..54089
 /note="similar to EST AI080470 (NID:g3416721) os71c05.x1"
misc feature 54088..54107
 /note="similar to EST AA121611 (NID:g1679226) zn78c08.r1"
repeat region 54089..54387
 /rpt_family="Alu"
misc feature 54390..54766
 /note="similar to EST AA101325 (NID:g1648130) zn73a10.s1"
misc feature 54401..54760
 /note="similar to EST AI080470 (NID:g3416721) os71c05.x1"
misc feature 54534..54754
 /note="similar to EST AA728785 (NID:g2750144) nx37h10.s1"
misc feature 54766..54776
 /note="match to EST W37475 (NID:g1319136) zc12e08.s1"
repeat region 55225..55523
 /rpt_family="Alu"
misc feature 55241..55714
 /note="similar to EST AI355155 (NID:g4095308) qt80g02.x1"
repeat region 55642..55691
 /rpt_family="L2"
misc feature 55915..56054
 /note="similar to EST AI821213 (NID:g5440292) ne09f10.y5"
misc feature 55915..55950
 /note="similar to EST AI807218 (NID:g5393784) wf38b11.x1"
repeat region 56154..56450
 /rpt_family="Alu"
repeat region 56897..57043
 /rpt_family="L2"
repeat region 57187..57364
 /rpt_family="L2"
repeat region 58089..58230
 /rpt_family="MIR"
misc feature 58262..59063
 /note="CpG_island (%GC=70.3, o/e=0.80, #CpGs=82)"
repeat region 58469..58496
 /rpt_family="GC_rich"
repeat region 59095..59713
 /rpt_family="MER4-group"
STS complement(59753..59931)
 /db_xref="GI:3800635"
misc feature 59753..59931
 /note="match to EST AA078521 (NID:g1838009)"
repeat region 60160..60466
 /rpt_family="Alu"
repeat region 60589..60796
 /rpt_family="MER4-group"
repeat region 60783..60807
 /rpt_family="MER4-group"
repeat region 60808..60970
 /rpt_family="MER4-group"
repeat region 60997..61139
 /rpt_family="MER4-group"
repeat region 61140..61443
 /rpt_family="Alu"
repeat region 61444..61802
 /rpt_family="MER4-group"
repeat region 62248..62299
 /rpt_family="L2"
repeat region 62419..62725
 /rpt_family="Alu"
misc feature 62704..62719

/note="match to EST AA846256 (NID:g2932396) ai83g05.s1"
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repeat_region 62928..63035
 /rpt_family="MER1_type"
repeat_region 62934..63047
 /rpt_family="MER1_type"
repeat_region 63154..63180
 /rpt_family="(TTG)n"
repeat_region 63181..63221
 /rpt_family="Alu"
repeat_region 63222..63442
 /rpt_family="Alu"
repeat_region 63472..63671
 /rpt_family="MaLR"
repeat_region 63672..64071
 /rpt_family="MER90"
misc_feature 63940..63944
 /note="similar to EST AI080470 (NID:g3416721) os71c05.x1"
repeat_region 64072..64525
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misc_feature 64216..64220
 /note="similar to EST AA728785 (NID:g2750144) nx37h10.s1"
repeat_region 64573..64822
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repeat_region 64884..65141
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repeat_region 65142..65444
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repeat_region 65445..65649
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repeat_region 65660..65700
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repeat_region 66669..66747
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repeat_region 68194..68633
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repeat_region 68639..69108
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repeat_region 69117..69137
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misc_feature 69382..69588
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misc_feature 69382..69648
 /note="similar to EST AA031509 (NID:g1501463) zk13a09.s1"
misc_feature 69383..69648
 /note="similar to EST AI032905 (NID:g3253858) ox19e05.s1"
misc_feature 69389..69648
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misc_feature 72025..72124
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repeat_region 74687..74850
 /rpt_family="MER4-group"
repeat_region 74890..75112
 /rpt_family="L1"
repeat_region 75246..75359
 /rpt_family="Alu"
repeat_region 76347..76448
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repeat_region 77147..77438
 /rpt_family="L2"
misc_feature 78090..78319
 /note="match to EST Y08472 (NID:g1620944)"
repeat_region 78095..78133
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repeat_region 78436..78541
 /rpt_family="MaLR"
repeat_region 78517..78824
 /rpt_family="MaLR"
repeat_region 79695..79857
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repeat_region 79895..80278
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repeat_region 80365..80428
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repeat_region 82445..82608
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repeat_region 82644..82950
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repeat_region 83277..83495
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repeat_region 84053..84354
 /rpt_family="Alu"
repeat_region 84564..84697
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repeat_region 84700..84821
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repeat_region 84848..85054
 /rpt_family="MaLR"
repeat_region 85105..85276
 /rpt_family="MaLR"
repeat_region 85558..85853
 /rpt_family="Alu"
misc_feature 86567..86673
 /note="similar to EST Y08714 (NID:g1620957)"
misc_feature 86567..86673
 /note="similar to EST Y08709 (NID:g1620946)"
misc_feature 86569..86673
 /note="similar to EST AW491691 (NID:g7061972)"
misc_feature 86578..86673
 /note="match to EST H11135 (NID:g875955) ym09b02.r1"
repeat_region 87271..87421

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87485..87561
repeat_region /rpt_family="MER1_type"
87565..87770
repeat_region /rpt_family="MER1_type"
87774..87886
repeat_region /rpt_family="MER1_type"
87960..88263
misc_feature /rpt_family="Alu"
88506..88621
misc_feature /note="similar to EST Y08714 (NID:g1620957)"
88506..88613
misc_feature /note="similar to EST AW491691 (NID:g7061972)"
88506..88613
misc_feature /note="match to EST H11135 (NID:g875955) ym09b02.r1"
88506..88613
misc_feature /note="similar to EST Y08709 (NID:g1620946)"
88683..88695
misc_feature /note="match to EST AA449630 (NID:g2163380) zx08f01.r1"
89129..89424
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90480..90775
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repeat_region /rpt_family="MIR"
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92331..92475
misc_feature /note="similar to EST Y08709 (NID:g1620946)"
92332..92476
misc_feature /note="similar to EST AW491691 (NID:g7061972)"
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misc_feature /note="match to EST H11135 (NID:g875955) ym09b02.r1"
92334..92475
misc_feature /note="match to EST R23506 (NID:g778394) yg29a10.r1"
92344..92475
misc_feature /note="match to EST F12201 (NID:g706543)"
93242..93497
misc_feature /note="similar to EST AW450196 (NID:g6990972)"
93389..93521
repeat_region /rpt_family="Alu"
94544..94564
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94589..94751
repeat_region /rpt_family="L2"
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misc_feature /note="match to EST F12201 (NID:g706543)"
95385..95558
misc_feature /note="match to EST R23506 (NID:g778394) yg29a10.r1"
95385..95490
misc_feature /note="similar to EST AW632612 (NID:g7389692)"
95385..95409
misc_feature /note="similar to EST Y08709 (NID:g1620946)"
97080..97145
misc_feature /note="match to EST R23506 (NID:g778394) yg29a10.r1"
97354..97665
repeat_region /rpt_family="Alu"
97878..98399
misc_feature /note="similar to EST AI355055 (NID:g4095208) qu16f03.x1"
97945..98499
misc_feature /note="similar to EST AI652234 (NID:g4736213) wb28a07.x1"
98119..98499
misc_feature /note="similar to EST AW197335 (NID:g6476565) xm38f04.x1"
98197..98233
repeat_region /rpt_family="L1"
98296..98333
repeat_region /rpt_family="AT_rich"

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repeat_region 99065..99189
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STS complement(99092..99389)
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repeat_region 99528..99643
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repeat_region 99974..100140
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repeat_region 101106..101126
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misc_feature 102384..102638
 /note="similar to EST AI695847 (NID:g4983747). wb79e04.x1"
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repeat_region 103487..103660
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repeat_region 104380..104463
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repeat_region 104553..104601
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repeat_region 104602..104716
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repeat_region 104717..104943
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repeat_region 104935..105044
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STS 105959..106152
 /db_xref="GI:1113458"
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repeat_region 107176..107282
 /rpt_family="MIR"
repeat_region 107378..107592
 /rpt_family="MER2_type"
repeat_region 107593..107709
 /rpt_family="MER2_type"
repeat_region 107710..107976
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repeat_region 108357..108641
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misc_feature 108566..108629
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misc_feature 108589..108629
 /note="match to EST AA603017 (NID:g2436878) np32a04.s1"
misc_feature 108589..108630
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repeat_region 108931..109243

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	/rpt_family="MER2_type"
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<u>misc_feature</u>	117635..118031
	/note="similar to EST AI206336 (NID:g3765008) qr21g05.x1"
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<u>repeat_region</u>	120611..121061
	/rpt_family="MER1_type"
<u>repeat_region</u>	121708..121920
	/rpt_family="MER1_type"
<u>repeat_region</u>	121926..122199
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<u>repeat_region</u>	122278..122405
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<u>repeat_region</u>	122609..122705
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<u>repeat_region</u>	126658..126682
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misc feature 126666..126678
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misc feature 126691..126983
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repeat region 127063..127544
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misc feature 127516..128007
 /note="similar to EST AI473680 (NID:g4326725) ta17a05.x1"
repeat region 129757..129821
 /rpt_family="(CA)n"
repeat region 129885..130065
 /rpt_family="MER2_type"
repeat region 130479..130500
 /rpt_family="AT_rich"
repeat region 130805..130893
 /rpt_family="L2"
repeat region 130964..131422
 /rpt_family="L2"
repeat region 131423..131722
 /rpt_family="Alu"
misc feature 131715..131731
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//

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Appendix e-1



Sequence Revision History

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Sequence Revision History				
Query	GI	Version	Update Date	Status
AC005586	8468933	2	Sep 30 2000 5:37	Live
AC005586	8468933	2	Jun 12 2000 8:30	Dead
AC005586	3907529	1	Nov 22 1998 18:11	Dead
AC005586	3510275	N/A	Sep 1 1998 18:04	Dead

Sequence "AC005586" was first seen at NCBI on Sep 1 1998 18:04

Revised: October 24, 2001.

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CCCCATCT
CACAGACATACGCT

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1: AC005586[gi:3510275]

LOCUS AC005586 128019 bp DNA HTG 01-SEP-1998
DEFINITION Homo sapiens clone DJ0584D14, *** SEQUENCING IN PROGRESS ***, 18
unordered pieces.
ACCESSION AC005586
VERSION AC005586 GI:3510275
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 128019)
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 128019)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT [WARNING] On Nov 22, 1998 this sequence was replaced by a newer
version gi:3907529.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2041: contig of 2041 bp in length
* 2042 2059: gap of unknown length
* 2060 4956: contig of 2897 bp in length
* 4957 4974: gap of unknown length
* 4975 8150: contig of 3176 bp in length
* 8151 8168: gap of unknown length
* 8169 10769: contig of 2601 bp in length
* 10770 10787: gap of unknown length
* 10788 15425: contig of 4638 bp in length
* 15426 15443: gap of unknown length
* 15444 18437: contig of 2994 bp in length
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BASE COUNT 34980 a 29241 c 29902 g 33591 t 305 others
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120661	gggtttcagc	cttctttgag	gttgttgtca	aacccagcct	gggtccactt	gcccagtggt
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120781	agcaccaggc	gaggagaatg	ggcagctaag	gctcaaactc	cctgatggct	tttaagcaag
120841	ggtttttaag	gcagggggtg	ggagggtttca	aaggggagtta	ggggctgagg	aatttctgga
120901	acttccttat	ccattttctg	gttccagctg	gtctgaggtc	tacgtgctgg	cattgtcacg
120961	tggtgacatt	ggtgggggtc	ctggctcctg	aaaaacaact	caaggatata	tgtcaagatg
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121441	cgggtttattc	attcatttcc	ccaattcatg	gttgtagagc	tagctagggtg	cctggaattt
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121681	caacatggag	aaaccctgtc	tctactaaaa	atacaaaatt	agccgggcat	ggtggtgcat
121741	gcctgtaatc	ccagctactc	ggcaggctga	ggcaggagaa	tcacttgaac	ccaggaggca
121801	gaagtgtcag	tgagccgaga	tcgcgccatg	gcaccccagc	ctgggcaaca	actctgtctc
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123301	tatttttttt	cttagtgga	ataggatccc	agaggttctc	cattctttcc	acctctgaaa
123361	tacccttgggt	catgggatgc	caatctggag	gaagtctgct	ctgtaagaag	gaaacaggcc
123421	cagagagtgg	aagtgacccc	caccgggtggg	ggtcctaatt	tctgaaaaac	aactcaagga

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123961	acctgggaaa	catagcaaga	ccccgtcttt	aaaaaaataa	acaggagaat	gagactccaa
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124201	gtatctttta	taaaaagtac	acatgaagtt	agtgacaaaa	tcgaatctca	gtccccagtt
124261	cctgctgtgc	tactgaggct	aaaccgcagc	cgggcctgtg	gcaaatgttt	aatcagctgt
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124381	cagcttctgt	ctgtatctac	ctcatgcccc	agaggcagct	tctagcagct	ccggagagca
124441	tcttgccagt	gggagttgac	ccagctgcgc	cccctttgag	ggagaagtgt	gaggaatttc
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127501 accaggctgg ctgttcatac cctgaggtag agttcttata accctgagtg gggagcgggt
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127981 ggagagtggg cacagtggg gtggccttgt gctgagtgg

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Revised: October 24, 2001.

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Appendix D

Express Mail No. EL844533597US
Date of Deposit: February 8, 2002
DOCKET NO. V0139/7038/HCL/MAT

ATTORNEY'S DOCKET NO.: V0139/7038 (HCL/MAT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Nicholas H. Heintz and Christopher R. Houchens
Serial No. 09/477,392
Filed: January 4, 2000
For: RIP60 NUCLEIC ACID AND POLYPEPTIDE SEQUENCES AND
USES THEREFOR
Examiner: Robert A. Zeman
Art Unit: 1645

COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231

DECLARATION OF NICHOLAS H. HEINTZ UNDER 37 C.F.R. § 1.131

Sir:

I, Nicholas H. Heintz, declare that:

1. I am an inventor of the above-identified patent application. I make this declaration in support of that application and in response to the Office Action (paper no. 12) dated October 9, 2001.
2. The purpose of this declaration is to establish reduction to practice of the claimed invention in a WTO member country prior to September 1, 1998, the date of deposit with GenBank of the sequence having Accession Number AC005586, by Sulston et al. This sequence was cited by the Examiner in the above-identified Office Action.
3. To establish reduction to practice of the claimed invention, I submit herewith a copy of the nucleic acid sequence of RIP60 as in my possession prior to September 1, 1998, as Exhibit 1. Nucleotides 19-2972 of the sequence in Exhibit 1 correspond to nucleotides 1-2954 of the nucleic acid sequence of RIP60 filed in the patent application (i.e., SEQ ID NO:1). The sequence of SEQ ID NO:1 is appended herewith as Exhibit 2. An alignment of the sequences in Exhibits 1 and 2

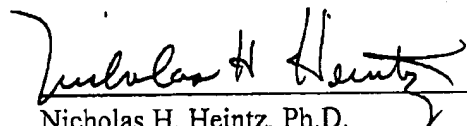
591594.1

was conducted using the "Blast 2 Sequences" tool found at the NCBI web site. The results of this alignment, appended herewith as Exhibit 3, demonstrate that there is 100% identity of these sequences in the regions listed above. The remaining 18 nucleotides upstream (i.e., 5') and 4 nucleotides downstream (i.e., 3') of the region of identity correspond to sequences from the vector used to clone the RIP60 nucleic acid sequence.

4. From Exhibit 1, one of ordinary skill in the art would recognize that I had reduction to practice of the claimed invention in a WTO member country prior to September 1, 1998.

I, the undersigned, declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under §1001 of title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this document and any patent which may issue from the above-identified patent application.

Date: Feb 6, 2002



Nicholas H. Heintz, Ph.D.
Department of Pathology
University of Vermont College of Medicine
Burlington VT 05405

EXHIBIT 1

Complete RIP60 Sequence Prior to September 1998

tatcgaattccggaattccgctgtttgtccagcttctcagagttgctgtgcagctcggatgtggcataggaaacagcaga
cacagggagaggggagcagcataaaggcactgtagggagcagtgccacattttctgcagaggaagaaccgatgctggaacgtc
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aaacagaacaaccatttaccctccttttcaaactagagaataaacatttgggttttagaaaaaaaaaaaaaaaaaaaaaa
aaaaaaaaaaaaaggcc

Appendix D

EXHIBIT 2

RIP60 Sequence as filed (i.e., SEQ ID NO:1)

cgctgtttgt ccagcttctc agagttgctg tgcagctcgg atgtggcata ggaaacagca
gacacagggg gagggcagca taaggcactg tagggagcag tggccacatt ttctgcagag
gaagaaccg atg ctg gaa cgt cgt tgc agg ggc ccc ctg gcc atg ggc ctg
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cgg ccc ttc ata tgc ggc aac tgt ggc cgg agc ttt gcc cag tgg gac
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acc gcc ccc cgg ccc ggt gga gat gcc gtc gac cgc ccc ttc cag tgt
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cgc cgc gtg cac acg ggc gag cgg ccc cac cag tgc ccc gag tgc ggg
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aag tcc aac ctc atc acc cac cgc aag agc cac atc cgg gac ggc gcc
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agccccctct tgcctccttc cacagctcag catgtcacgg caaggactgc cgcattgggtg
atggaggggc agctgagggg aagtgtctgg tgagtttctt ttctccattt ctagcatatg
acacctggcc totgcttgag cacttaggtg acaggaactt ccgcacctcc tgaggccctg
gatgattcta attgttagaa attctaattg ttagaaatcc ttccttataa tgaatgaatt
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aaccatttac cctcctttt caaactagag aataaacatt tggttttaga aaaaaaaaaa
aaaaaaaaaa aaaaaaaaaa aaa

NCBI

Entrez

Blast 2 sequences

BLAST

Help

Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☐

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from to:

```
tatcgaattccggaattccgctgtttgtccagcttctcagagttgctgtgcagctcggat
gtggcataggaacagcagacacagggagagggcagcataaaggcactgtaggagcagt
gccacattttctgcagaggaagaaccgatgctggaacgctcgttgaggggcccccctggcc
atgggcctggcccagccccgactcctttctggggccctcccaggagtcaccccagaccctg
gggaaggagtcccgcgggctgaggcaacaaggcacgtcagtggccagctctggtgccaa
gccccaggcaggggcccatcgctgtgccactgtcgaaggcacttccctggctgggtggct
ctgtggcttcacacccgcgggtccaggcccgctgccccttgccctgacctgagtggtg
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from to:

```
cgctgtttgt ccagcttctc agagttgctg tgcagctcgg atgtggcata
ggaaacagca      60
gacacagga gagggcagca taaggcactg tagggagcag tggccacatt
ttctgcagag     120
gaagaaccg atg ctg gaa cgt cgt tgc agg ggc ccc ctg gcc atg
ggc ctg      171
```

RIP60
Sequence in
inventor's possession
prior to September 1998

RIP60
Sequence as filed
in patent application
(SEQ ID No: 1)

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov

Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)

Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

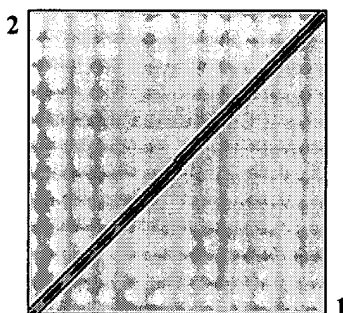
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: Mismatch: gap open: gap extension:

x dropoff: **50** expect: **1.0000** wordsize: **11** Filter ☐ Align ☐

Sequence 1 |cl|seq 1 Length 2976 (1 .. 2976)

Sequence 2 lcl|seq 2 Length 2954 (1 .. 2954)



comparison of
sequence prior to
September 1998
and sequence as filed
SEQ ID No: 1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 5680 bits (2954), Expect = 0.0

Identities = 2954/2954 (100%)

Strand = Plus / Plus

9/98

```
Query: 19      cgctgtttgtccagcttctcagagttgctgtgcagctcggatgtggcataggaaacagca 78
               |||
Sbjct: 1       cgctgtttgtccagcttctcagagttgctgtgcagctcggatgtggcataagaaaacagca 60
```

Sbjct: 1 cgctgtttgtccagcttctcagagttgctgtgcagctcggatgtggcataggaaacagca 60
filed

Query: 79 gacacagggagaggggcagcataaggcactgtagggagcagtggccacattttctgcagag 138

Sbjct: 61 gacacaggggagagggcagcataaggcactgtagggagcagtgccacattttctgcagag 120

Query: 139 gaagaaccgatgctggaacgtcgttgacagggggccccctggccatgggcctggcccagccc 198

Sbjct: 121 gaagaaccgatgctggaacgtcggtgcagggggccccctggccatgggcctggcccagccc 180

Query: 199 cgactcctttctgggccctcccaggaagtcaccccagaccctgggggaaggagtcctcgccggg 258

Sbjct: 181 cgactcctttctgggccctcccaggagtcaccccagaccctggggaaggagtcgccggg 240

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Sbjct: 241 ctgaggcaacaaggcacgtcagtgcccagtcctggtgcccaagccccaggcagggcccat 300

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Query: 379 cggtgccaggccccggctgcccttgccctgccctgagtgtggccgctcgtttcgccatgcc 438
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Query: 2959 aaaaaaaaaaaaaa 2972
|||||

Sbjct: 2941 aaaaaaaaaaaaaa 2954

CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 83
Number of Sequences: 0
Number of extensions: 83
Number of successful extensions: 71
Number of sequences better than 1.0: 1
length of query: 2954
length of database: 4,677,375,331
effective HSP length: 25
effective length of query: 2929
effective length of database: 4,674,138,981
effective search space: 13690553075349
effective search space used: 13690553075349
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 23 (44.9 bits)



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1 Genetic Mapping

Genetic Mapping

RNase A stock solution (DNase-free), 2 mg/ml

Dissolve RNase A (e.g., Sigma) in DEPC-treated H₂O (UNIT 7.1 to 2 mg/ml). Boil 10 min in a 100°C water bath. Store ≤1 year at 4°C.

The activity of the enzyme varies from lot to lot; therefore, prepare several 10-ml aliquots of each dilution to facilitate standardization.

SDS, 20%

Dissolve 20 g SDS (sodium dodecyl sulfate or sodium lauryl sulfate) in H₂O to 100 ml total with stirring (it may be necessary to heat the solution slightly to fully dissolve the powder). Filter sterilize using a 0.45-μm filter.

SOC medium

35 g yeast extract

20 g tryptone

0.5 g NaCl

2.5 ml 1 M KCl

H₂O to 960 ml

Adjust pH to 7.0 with 5 M NaOH (~0.2 ml)

Autoclave 25 min

Cool to 50°C

Add the following sterile ingredients:

10 ml 1 M MgCl₂ (10 mM final)

10 ml 1 M MgSO₄ (10 mM final)

20 ml 1 M glucose (20 mM final)

Store <1 year at 4°C

1 M glucose stock should be sterilized by filtration.

Sodium acetate, 3 M

408 g sodium acetate trihydrate (NaC₂H₃O₂·3H₂O)

800 ml H₂O

Adjust pH to 5.2 with 3 M acetic acid

Add H₂O to 1 liter

Sodium acetate buffer, 0.2 M

Solution A: 11.55 ml glacial acetic acid/liter (0.2 M).

Solution B: 27.2 g sodium acetate (NaC₂H₃O₂·3H₂O)/liter (0.2 M).

Referring to Table A.2D.3 for desired pH, mix the indicated volumes of solutions A and B, then dilute with H₂O to 200 ml. (See Potassium acetate buffer recipe for further details.)

CAUTION: *Glacial acetic acid is hazardous; see APPENDIX 2 for safety guidelines.*

Sodium phosphate buffer, 0.2 M

Solution A: 27.6 g NaH₂PO₄·H₂O per liter (0.2 M).

Solution B: 53.65 g Na₂HPO₄·7H₂O per liter (0.2 M).

Referring to Table A.2D.4 for desired pH, mix the indicated volumes of solutions A and B, then dilute with H₂O to 200 ml. (Also see Potassium phosphate buffer recipe for further details.)

SSC (sodium chloride/sodium citrate), 20×

175 g NaCl (3 M)

88 g trisodium citrate dihydrate Na₃C₆H₅O₇·2H₂O (0.3 M)

H₂O to 800 ml

Adjust pH to 7.0 with 1 M HCl

Add H₂O to 1 liter